A1 * cont.

large excess) and removing the RNA-DNA complexes. This method relies on the RNA-DNA hybridization taking place with all the species and members of the cDNA unseparated.

IN THE CLAIMS:

Please cancel claims 9 and 33-36 without prejudice

Please amend the claims as follows:

1. (amended) A method for constructing a normalized full-length cDNA library of genes of low expression, comprising:

(a) constructing a non-normalized cDNA library from an RNA sample, wherein said RNA sample contains different species of RNA of different amounts, wherein said non-normalized cDNA library contains a plurality of members;

A2

(b) separating the members of said non-normalized cDNA library;

(c) constructing a labeled probe library from said RNA sample;

(d) hybridizing a labeled probe library to said non-normalized cDNA library, whereby each individual member of said non-normalized cDNA library is hybridized to a differential of the amount of labeled probe of said labeled probe library;

(e) identifying the individual members of said non-normalized cDNA library hybridized with lower amounts of labeled probe; and

(f) pooling the individual members of said non-normalized cDNA library identified in step (e) in a collection;

whereby said collection is said normalized full-length cDNA library of genes of low expression.

A3

10. (amended) The method according to Claim 1, wherein said constructing of cDNA from said RNA sample comprises catalyzing a reverse

A3 cont.

transcription reaction for each species of said RNA sample, wherein said catalyzing takes place under conditions permissible for catalyzing a reverse transcription reaction.

14. (amended) The method according to Claim 13, further comprising:

amplifying each member of said non-normalized cDNA library,

wherein said amplifying comprises growing each said host cell containing cDNA, wherein said amplifying step is subsequent to said transforming and prior to said hybridizing.

15. (amended) A method for constructing a normalized cDNA library, comprising:

(a) constructing a non-normalized cDNA library from an RNA sample, wherein said RNA sample contains different species of RNA of different amounts, wherein each member of said non-normalized cDNA library is separate from other members;

A4

(b) identifying the relative amounts of each member of said non-normalized cDNA library represented in said RNA sample;

(c) dividing the members of said non-normalized cDNA library into groups; wherein one group of members of said non-normalized cDNA library is represented in lower amounts by said RNA sample and one or more groups of members of said non-normalized cDNA library is represented in higher amounts by said RNA sample;

(d) selecting a first sub-group of said one or more groups of members of said non-normalized cDNA library represented in higher amounts by said RNA sample;

(e) identifying the members in said group of members of said non-normalized cDNA library represented in higher amounts by said RNA sample, which is not represented within said first sub-group of members selected from said group of members;

(f) forming a second sub-group of members from the members identified in step (e) and repeating step (e) until every member of said group of members of said non-normalized cDNA library represented in higher amounts by said RNA sample has been selected within a sub-group of members;

A4 cont.

(g) pooling the members of said group of members of said non-normalized cDNA library represented in lower amounts by said RNA sample and the members of every sub-group selected in a collection;

whereby said collection is said normalized cDNA library.

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24. (amended) The method according to Claim 15, wherein said constructing a non-normalized cDNA library from an RNA sample comprises catalyzing a reverse transcription reaction for each species of said RNA sample, wherein said catalyzing takes place under conditions permissible for catalyzing a reverse transcription reaction.

A5

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28. (amended) The method according to Claim 27, further comprising:

amplifying each member of said non-normalized cDNA library,

wherein said amplifying comprises growing each said host cell containing cDNA, wherein said amplifying step is subsequent to said transforming and prior to said identifying of step (b).

A6

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31. (amended) The method according to Claim 15, further comprising:

sequencing a member of said group members of said non-normalized cDNA library represented in lower amounts by said RNA sample and a member of every sub-group selected prior to said pooling, wherein a sufficient number of nucleotides are sequenced to identify members that are represented no more than once; and

pooling unique members determined by said sequencing.

A7

32. (amended) A method for constructing a normalized cDNA library of genes of low –expression in a species, comprising:

(a) constructing a non-normalized cDNA library from an RNA sample from a plurality of different tissues, developmental stages or individuals from the same species of organism, wherein said RNA sample contains different species of RNA of different amounts, wherein each member of said non-normalized cDNA library is separate from other members;

A7 cont.

(b) identifying the relative amounts of each member of said non-normalized cDNA library represented in said RNA sample;

(c) pooling the members of said non-normalized cDNA library represented in lower amounts by said RNA sample in a collection;

whereby said collection is said normalized cDNA library of genes of low expression for a species of organism.

Please add the following new claims 37-46 as follows:

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37. The method according to claim 32, wherein RNA from substantially every cell type and/or tissue from the same species of organism is used.

38. The method according to claim 2, wherein said RNA sample is from a plurality of different cell types and/or tissue.

A8

39. The method according to claim 2, wherein said RNA sample is from a plurality of different individuals from the same species of organism.

40. The method according to claim 1, wherein said labeled probe library from said RNA sample is from another cell type or tissue of the same organism.